

AMENDMENTS TO THE SPECIFICATION

Please amend the paragraph beginning on line 25 of page 5 as follows:

It will be appreciated that in derivatives of LT-A, such as fragments, or in LT-A proteins of different *E. coli* strains, the amino acid residue to be mutated is that which corresponds to Ala-72 as defined for LT-A in Domenighini et al. [Molec. Microbiol. (1995) 15:1165-1167]. Ala-72 is located on the second turn of the alpha-helix in LT-A and faces the NAD binding site. An alignment of amino acid sequence entries for enterotoxin A subunits is shown in Figure 1 of Domenighini and reproduced as FIG. 12 herein. The correct sequences of LTp, LTh, LT-IIa and LT-IIb as given in Domenighini are as follows:

LTp:

NGDRLYRADS RPPDEIKRSGGLMPRGHNEYFDRQTQMNINLYDHARGTQTGFVRY
DDGYVSTSLSLRSAHLAQSI LSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQE
VSALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFP
PDHQA WREEPWIHHAPQGC GNSSRTITGDT CNEETQNLSTIYLR EYQSKVKRQIFSD
YQSEVDIYNRIRDEL (SEQ ID NO:1)

LTh:

NGDKLYRADS RPPDEIKRSGGLMPRGHNEYFDRQTQMNINLYDHARGTQTGFVRY
DDGYVSTSLSLRSAHLAQSI LSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQE
VSALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFP
PDHQA WREEPWIHHAPQGC GNSSRTITGDT CNEETQNLSTIYLRKYQSKVKRQIFSD
YQSEVDIYNRIRNEL (SEQ ID NO:2)

LT-IIa:

NDFFRADS RTPDEIRRAGGL LPRGQQEAYERQTPININLYEHARGTVTG NTRYNDG
YVSTTVTLRQAHLIGQNILGSYNEYYIYVVAPAPNLFDVNGVLGRYSPYPSENEFAA
LGGIPLSQIIGWYRVSFGAIEGGMQRNRDYRGDLFRGLTVAPNEDGYQLAGFPSNFP

AWREMPWSTFAPEQCVNNKEFKGGVCISATNVLSKYDLMNFKLLKRRLALTFF
MSEDDFIGVHGERDEL (SEQ ID NO:3)

LT-IIb:

NDYFRADSRTTPDEVRRSGGLIPRGQDEAYERQTPININLYDHARGTATGNTRYNDG
YVSTTTTLRQAHFLGQNMLGGYNEYIYVVAAPNLFDVNGVLGRYSPYSENEF
AALGGIPLSQIIGWYRVSFGEIEGGMHRNRDYRRDLFRGLSAAPNEDGYRIAGFPDG
FPAWEEVPWREFAPNSCLPNNKASSDTTCASLTNKLSDHDLADFKKYIKRKFTLMR
INNDGFFSNNGGKDEL (SEQ ID NO:4)